

## 1/49

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu-Ser  
 65 70 75 80  
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255-

tac gct taa

Tyr Ala

777

&lt;210&gt; 2

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Manihot esculenta

&lt;400&gt; 2

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

<400> 3																
atg gca ttc gct cat ttt gtt ctt att cat acc ata tgc cac ggt gca	48															
Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala																
1 5 10 15																
tgg att tgg cac aag ctc aaa ccc ctc ctt gag gca ctt ggc cac aag	96															
Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys																
20 25 30																
gtt act gca ctg gac ctt gca gca agc ggc gtt gac cca agg caa att	144															
Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile																
35 40 45																
gag gag att ggc tca ttt gat gag tat tot gaa ccc ttg ttg acg ttc	192															
Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe																
50 55 60																
ttg gag gca ctc cct cca ggg gaa aag gtg att ctg gtt ggc gag agc	240															
Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser																
65 70 75 80																
tgt gga gga ctc aat ata gca att gct gct gat aaa tac tgt gaa aag	288															
Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys																
85 90 95																
att gca gct gct gtt ttc cac aat tca gta ttg cca gac acc gag cac	336															
Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His																
100 105 110																

tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg 384  
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp  
 115 120 125

aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata-act 432  
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr  
 130 135 140

gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt 480  
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu  
 145 150 155 160

tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga 528  
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly  
 165 170 175

tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa 576  
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu  
 180 185 190

ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa 624  
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu  
 195 200 205

ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca 672  
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro  
 210 215 220

gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca 720  
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr  
 225 230 235 240

aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat 768  
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr  
 245 250 255

aat tga 774  
 Asn

<210> 4

<211> 257

<212> PRT

<213> Hevea brasiliensis

&lt;400&gt; 4

Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser  
 65 70 75 80  
 Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys  
 85 90 95  
 Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His  
 100 105 110  
 Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp  
 115 120 125  
 Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr  
 130 135 140  
 Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu  
 145 150 155 160  
 Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly  
 165 170 175  
 Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu  
 180 185 190  
 Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu  
 195 200 205  
 Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro  
 210 215 220  
 Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr  
 225 230 235 240  
 Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr  
 245 250 255  
 Asn

&lt;210&gt; 5

&lt;211&gt; 777

&lt;212&gt; DNA

<213> *Manihot esculenta*

&lt;220&gt;

<223> cDNA coding for Modified SHNL involving  
 a replacement of Gly by Asp at position 165

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (777)

&lt;400&gt; 5

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	
1 5 10 15	
tggtg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	
20 25 30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	
35 40 45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	
50 55 60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	
65 70 75 80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa	288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys	
85 90 95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac	336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His	
100 105 110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg	384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp	
115 120 125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc	432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile	
130 135 140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc aco	480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr	
145 150 155 160	

aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
                   165                  170                  175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
                   180                  185                  190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
                   195                  200                  205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
                   210                  215                  220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
                   225                  230                  235                  240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                   245                  250                  255

tac gct taa 777  
 Tyr Ala

<210> 6  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
       a replacement of Gly by Asp at position 165

<400> 6  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
       1                  5                  10                  15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
                   20                  25                  30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
                   35                  40                  45



Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp-Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

&lt;210&gt; 7

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;220&gt;

<223> cDNA coding for Modified SHNL involving  
 a replacement of Gly by Glu at position 165

&lt;400&gt; 7

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His-Lys  
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala-Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190  
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 tac gct taa 777  
 Tyr Ala

<210> 8  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Gly by Glu at position 165

<400> 8  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

&lt;210&gt; 9

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 9

ggggaattca tgggttactgc acacttcggtt ctgattcac

39

&lt;210&gt; 10

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 10

gggaagcttt taagcgtatg catcagcaac ttcttcgag

39

<210> 11

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gggggggggc atatggttac tgcacacttc gttctgattc acac

44

<210> 12

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gggggatcct taagcgatg catcagcaac ttcttcag

39

<210> 13

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

cgtgaaaacc tgttcaccaa atgcactgat gaagaatatg aactggcaaa aatg

54

<210> 14

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

&lt;400&gt; 14

catttttgcc agttcatatt cttcatcagt gcatttgggtg aacaggtttt cacg 54.

&lt;210&gt; 15

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;220&gt;

<223> cDNA coding for Modified SHNL involving  
a replacement of Val by Leu at position 173

&lt;400&gt; 15

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cg t gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cg t gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg ctg atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cg t ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

&lt;210&gt; 16

&lt;211&gt; 258

&lt;212&gt; PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving  
a replacement of Val by Leu at position 173

<400> 16

Met	Val	Thr	Ala	His	Phe	Val	Leu	Ile	His	Thr	Ile	Cys	His	Gly	Ala
1				5				10						15	
Trp	Ile	Trp	His	Lys	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys
			20					25					30		
Val	Thr	Ala	Leu	Asp	Met	Ala	Ala	Ser	Gly	Ile	Asp	Pro	Arg	Gln	Ile
		35					40					45			
Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe
	50					55				60					
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser
65					70					75					80
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys
				85					90					95	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His
		100						105					110		
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
		115					120					125			
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130					135					140				
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
145					150					155					160
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Leu	Met	Arg	Lys
			165						170					175	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
		180						185					190		
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
	195						200					205			
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
	210					215					220				
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
225					230					235					240
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
			245						250					255	
Tyr	Ala														

<210> 17

<211> 45



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

ggcgaatatg aactggcaaa aatgnnnatg cgcaagggt ctctg 45

<210> 18

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 18

cagagagccc ttgcgcatnn ncatttttgc cagttcatat tcgcc 45

<210> 19

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1).. (777)

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Met by Leu at position 174

<400> 19

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcc ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt ttg cgc aag 528  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys  
 165 170 175  
 ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 18/49

210	215	220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg			720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu			
225	230	235	-240
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca			768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala			
245	250	255	
tac gct taa			777
Tyr Ala			

<210> 20  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Met by Leu at position 174

<400> 20  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys

165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

<210> 21  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> -(1).. (777)

<220>  
 <223> cDNA coding for Modified SHNL(SHNL Actmt022-G12) involving  
 a replacement of Lys by Asn at position 21

<400> 21  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 tgg att tgg cac aat ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac-aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tgc ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 21/49

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa  
 Tyr Ala

777

&lt;210&gt; 22

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Manihot esculenta

&lt;220&gt;

<223> Modified SHNL (SHNL Actmt022-G12) involving  
 a replacement of Lys by Asn at position 21

&lt;400&gt; 22

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

<210> 23

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 23

ggcgcatgga tttggcacnn nctgaaaccg gccctggaa

39

<210> 24

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 24

ttccagggcc ggtttcaghn ngtgccaaat ccatgcgcc

39

<210> 25

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving  
 a replacement of Lys by Glu at position 21

&lt;400&gt; 25

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

tgg att tgg cac gaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175



ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa-gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa 777  
 Tyr Ala

<210> 26  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Lys by Glu at position 21

<400> 26  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

	85		90		95										
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His
	100						105					110			
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp
	115						120					125			
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile
	130						135					140			
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr
	145						150				155				160
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys
			165							170					175
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu
			180						185					190	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp
		195						200					205		
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys
		210					215					220			
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu
	225					230				235					240
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala
			245						250					255	
Tyr	Ala														

&lt;210&gt; 27

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (777)

&lt;220&gt;

<223> cDNA coding for Modified SHNL involving  
a replacement of Lys by Asp at position 21

&lt;400&gt; 27

atg	ggt	act	gca	cac	ttc	gtt	ctg	att	cac	acc	att	tgt	cac	ggc	gca	48
Met	Val	Thr	Ala	His	Phe	Val	Leu	Ile	His	Thr	Ile	Cys	His	Gly	Ala	
1					5						10				15	

tgg	att	tgg	cac	gac	ctg	aaa	cgc	gcc	ctg	gaa	cgt	gct	ggc	cac	aaa	96
Trp	Ile	Trp	His	Asp	Leu	Lys	Pro	Ala	Leu	Glu	Arg	Ala	Gly	His	Lys	

20	25	30	
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att			144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile			
35	40	45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc			192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe			
50	55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc			240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa			288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
85	90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac			336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			
100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg			384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc			432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag			528
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys			
165	170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
180	185	190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa 777  
 Tyr Ala

<210> 28  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Lys by Asp at position 21

<400> 28  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

&lt;210&gt; 29

&lt;211&gt; 777

&lt;212&gt; DNA

<213> *Manihot esculenta*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;220&gt;

<223> cDNA coding for Modified SHNL involving  
 a replacement of Lys by Asn at position 21

&lt;400&gt; 29

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

tgg att tgg cac aac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu	Gln	Ile	Asn	Ser	Phe	Asp	Glu	Tyr	Ser	Glu	Pro	Leu	Leu	Thr	Phe		
50						55					60						
ctg	gaa	aaa	ctg	ccg	caa	ggc	gaa	aag	gtt	atc	att	gtt	ggt	gaa	agc	240	
Leu	Glu	Lys	Leu	Pro	Gln	Gly	Glu	Lys	Val	Ile	Ile	Val	Gly	Glu	Ser		
65					70				75						80		
tgt	gca	ggc	ctg	aac	att	gct	att	gct	gct	gat	cgt	tac	gtt	gac	aaa	288	
Cys	Ala	Gly	Leu	Asn	Ile	Ala	Ile	Ala	Ala	Asp	Arg	Tyr	Val	Asp	Lys		
				85					90					95			
att	gca	gct	ggc	gtt	ttc	cac	aac	tcc	ctg	ctg	ccg	gac	acc	gtt	cac	336	
Ile	Ala	Ala	Gly	Val	Phe	His	Asn	Ser	Leu	Leu	Pro	Asp	Thr	Val	His		
			100					105						110			
agc	ccg	tct	tac	act	gtt	gaa	aag	ctg	ctg	gaa	tgc	ttc	ccg	gac	tgg	384	
Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
			115					120					125				
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
			130					135					140				
act	acc	atg	aaa	ctg	ggt	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
			145					150					155		160		
aaa	tgc	act	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Thr	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165					170					175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	ccg	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
				180					185					190			
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
				195					200					205			
aaa	ata	ttc	ctg	ccg	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
				210					215					220			
ccg	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		

225                      230                      235                      240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245                      250                      255-

tac gct taa 777

Tyr Ala

<210> 30

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Lys by Asn at position 21

<400> 30

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1                      5                      10                      15

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20                      25                      30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35                      40                      45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50                      55                      60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65                      70                      75                      80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85                      90                      95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100                      105                      110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115                      120                      125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130                      135                      140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145                      150                      155                      160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165                      170                      175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180                      185                      190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195	200	205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys		
210	215	220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu		
225	230	235
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala		
245	250	255
Tyr Ala		

&lt;210&gt; 31

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (777)

&lt;220&gt;

&lt;223&gt; cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

&lt;400&gt; 31

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca	48
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala	

1

5

10

15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa	96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys	

20

25

30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att	144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile	

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc	192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe	

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc	240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser	

65

70

75

80



tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
                     85                                    90                                    95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
                     100                                    105                                    110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
                     115                                    120                                    125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
                     130                                    135                                    140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
                     145                                    150                                    155                                    160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg atg cgc aag 528  
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys  
                     165                                    170                                    175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
                     180                                    185                                    190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
                     195                                    200                                    205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
                     210                                    215                                    220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
                     225                                    230                                    235                                    240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                     245                                    250                                    255

tac gct taa

777

Tyr Ala

&lt;210&gt; 32

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;223&gt; Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

&lt;400&gt; 32

```

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
  1             5             10             15
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
      20             25             30
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
      35             40             45
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
      50             55             60
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
      65             70             75             80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
      85             90             95
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
      100            105            110
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
      115            120            125
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
      130            135            140
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
      145            150            155            160
Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys
      165            170            175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
      180            185            190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
      195            200            205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
      210            215            220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
      225            230            235            240
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
      245            250            255

```

Tyr Ala

<210> 33

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 33

tatgaactgg caaaaatgct gctgcgcaag ggctctctgt tc

42

<210> 34

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 34

gaacagagag ccctigcgca gcagcatttt tgccagttca ta

42

<210> 35

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173  
and Met by Leu at position 174

<400> 35

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1	5	10	15	
tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa				96
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys				
20		25	30	
ggt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att				144
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile				
35		40	45	
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc				192
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe				
50		55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc				240
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser				
65		70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa				288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys				
85		90	95	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac				336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His				
100		105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg				384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp				
115		120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc				432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile				
130		135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc				480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr				
145		150	155	160
aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg ctg cgc aag				528
Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys				
165		170	175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa				576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu				
180		185	190	

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
           195                          200                          205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
           210                          215                          220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
           225                          230                          235                          240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                           245                          250                          255

tac gct taa 777  
 Tyr Ala

<210> 36  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
       replacement of Gly by Glu at position 165 and Val by Leu at position 173  
 and Met by Leu at position 174

<400> 36  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
       1                          5                          10                          15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
           20                          25                          30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
           35                          40                          45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
           50                          55                          60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
           65                          70                          75                          80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
                           85                          90                          95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

tgaaaacctg ttacacaaat gcnnngatgg cgaatatgaa ctggc

45

<210> 38

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

gccagttcat attgccatc nnnngcatttg gtgaacaggt ttcca

45

<210> 39  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <223> cDNA coding for Modified SHNL involving  
 a replacement of Thr by Asp at position 163

<220>  
 <221> CDS  
 <222> (1).. (777)  
 <223>

<400> 39  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser	Pro	Ser	Tyr	Thr	Val	Glu	Lys	Leu	Leu	Glu	Ser	Phe	Pro	Asp	Trp		
	115						120					125					
cgt	gac	aca	gaa	tat	ttc	acg	ttc	acc	aac	atc	act	ggc	gaa	acc	atc	432	
Arg	Asp	Thr	Glu	Tyr	Phe	Thr	Phe	Thr	Asn	Ile	Thr	Gly	Glu	Thr	Ile		
	130					135					140						
act	acc	atg	aaa	ctg	ggt	ttc	gtt	ctg	ctg	cgt	gaa	aac	ctg	ttc	acc	480	
Thr	Thr	Met	Lys	Leu	Gly	Phe	Val	Leu	Leu	Arg	Glu	Asn	Leu	Phe	Thr		
145					150					155				160			
aaa	tgc	gat	gat	ggc	gaa	tat	gaa	ctg	gca	aaa	atg	gtt	atg	cgc	aag	528	
Lys	Cys	Asp	Asp	Gly	Glu	Tyr	Glu	Leu	Ala	Lys	Met	Val	Met	Arg	Lys		
				165					170					175			
ggc	tct	ctg	ttc	caa	aac	gtt	ctg	gct	cag	cgt	cgc	aag	ttc	act	gaa	576	
Gly	Ser	Leu	Phe	Gln	Asn	Val	Leu	Ala	Gln	Arg	Pro	Lys	Phe	Thr	Glu		
			180					185					190				
aaa	ggc	tac	ggc	tct	atc	aag	aaa	gtt	tat	att	tgg	acc	gat	caa	gac	624	
Lys	Gly	Tyr	Gly	Ser	Ile	Lys	Lys	Val	Tyr	Ile	Trp	Thr	Asp	Gln	Asp		
	195					200					205						
aaa	ata	ttc	ctg	cgc	gac	ttc	caa	cgc	tgg	caa	att	gca	aac	tac	aaa	672	
Lys	Ile	Phe	Leu	Pro	Asp	Phe	Gln	Arg	Trp	Gln	Ile	Ala	Asn	Tyr	Lys		
	210					215					220						
cgc	gac	aag	gtt	tat	cag	gtt	caa	ggc	ggc	gat	cac	aag	ctg	cag	ctg	720	
Pro	Asp	Lys	Val	Tyr	Gln	Val	Gln	Gly	Gly	Asp	His	Lys	Leu	Gln	Leu		
225					230					235				240			
aca	aaa	act	gaa	gaa	gta	gct	cac	att	ctg	caa	gaa	gtt	gct	gat	gca	768	
Thr	Lys	Thr	Glu	Glu	Val	Ala	His	Ile	Leu	Gln	Glu	Val	Ala	Asp	Ala		
			245						250					255			
tac	gct	taa														777	
Tyr	Ala																

<210> 40  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta



&lt;220&gt;

<223> Modified SHNL involving  
a replacement of Thr by Asp at position 163

&lt;400&gt; 40

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160

Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

Tyr Ala

<210> 41  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <223> cDNA coding for Modified SHNL involving  
 a replacement of Thr by Glu at position 163

<220>  
 <221> CDS  
 <222> (1).. (777)  
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<400> 41  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca

48

43/49



Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160

Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp-Ala  
 245 250 255

Tyr Ala

<210> 43

<211> 777

<212> DNA

<213> *Manihot esculenta*

<220>

<223> cDNA coding for Modified SHNL involving  
 a replacement of Thr by Ser at position 163

<220>

<221> CDS

<222> (1).. (777)

<223>

<400> 43

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65	70	75	80	
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa				288
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys				
85		90	95 -	
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac				336
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His				
100	105		110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tgc ttc ccg gac tgg				384
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp				
115	120		125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc				432
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile				
130	135		140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc				480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr				
145	150	155	160	
aaa tgc tct gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag				528
Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys				
165	170		175	
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa				576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu				
180	185		190	
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac				624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp				
195	200		205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa				672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys				
210	215		220	
ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg				720
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu				
225	230	235	240	
aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca				768
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala				
245	250		255	

tac gct taa  
Tyr Ala

777

<210> 44  
<211> 258  
<212> PRT  
<213> Manihot esculenta

<220>  
<223> Modified SHNL involving  
a replacement of Thr by Ser at position 163

<400> 44

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys  
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110



Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
245 250 255

Tyr Ala